



003300-883.ST25

10/019566
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SEQUENCE LISTING

<110> Leif, Leif

<120> RECOMBINANT ADENOVIRUS

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<140> US 10/019,566

<141> 2002-03-28

<150> SE 9902601-5

<151> 1999-07-06

<150> US 60/143,632

<151> 1999-07-14

<150> PCT/SE00/01390

<151> 2000-06-30

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<301> Hoppe HJ, Barlow PN, Reid KBM

<302> A parallel three stranded a-helical bundle at the nucleation site of collagen triple-helix formation

<303> FEBS Letters

<304> 344

<306> 191-195

<307> 1994

<400> 1

Pro Asp Val Ala Ser Leu Arg Gln Gln Val Glu Asp Leu Gln Gly Gln

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Phe Pro Asn Gly

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<301> Harbury PB, Zhang T, Kim PS, Albert T

<302> A switch between two-, three-, and four-stranded coiled coils in GCN4 leucine zipper mutants

<303> Science

<304> 262

<306> 1401-1407
 <307> 1993-11-26

<400> 2
 Met Lys Gln Ile Gly Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr
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 <301> Brinkmann U, Buchner J, Pastan I
 <302> Independent domain folding of Pseudomonas exotoxin and single
 chain immunotoxins: Influence of interdomain connections
 <303> Proc. Natl. Acad. Sci. US
 <304> 89
 <306> 3075-3079
 <307> 1992

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 Ala Ser Gly Gly Pro Glu
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 <302> Independent domain folding of Pseudomonas exotoxin and single
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 <303> Proc. Natl. Acad. Sci. US
 <304> 89

<306> 3075-3079

<307> 1992

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Ala Ser Thr Pro Glu Pro Asp Pro
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<301> Dengl JL, Wensel TG, Morrison SL, Streyer L, Herzenberg LA,
and Oi T

<302> Segmental flexibility and complement fixation of genetically
engineered chimeric human, rabbit and mouse antibodies

<303> EMBO Journal

<304> 7

<306> 1989

<307> 1988

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Thr Pro Leu Gly Asp Thr Thr His Thr Ser Gly
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<212> PRT

<213> Adenovirus type 5

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<301> Stouten PFW, Sander C, Ruigrok WH, Cusack S

<302> New triple-helical model for the shaft of the adenovirus fibre

<303> Journal of molecular biology

<304> 226

<306> 1073-1084

<307> 1992

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Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
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<301> Fisher-Fantuzzi L and Vesco C

<302> Cell-Dependent Efficiency of Reiterated Nuclear Signals in a
Mutant Simian Virus 40 Oncoprotein Targeted to the Nucleus

<303> Molecular Cell Biology

<304> 8

<306> 5495-5503

<307> 1992

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Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu Val Phe Leu Ile

35

40

45

Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser Gly Arg Tyr Ser

50

55

60

Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe Thr Ile Thr Ala

65

70

75

80

Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala Leu Gly Gly Val

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Met Val Lys Pro

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Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu

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30

Ala Thr Gly Phe Phe Pro Asp His Val Glu Lys Ser Trp Trp Val Asn

35

40

45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys

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55

60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu

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70

75

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Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys

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tatgcactcg agtaaaagaat cgtttggttt atgtttcaac gtgtttattt ttc 53

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<222> (1)...(1746)
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      130-1200 Fiber shaft
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1201-1746 Fiber knob

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tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc	96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro	
20 25 30	
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct	144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser	
35 40 45	
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Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu	
50 55 60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser	
65 70 75 80	
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn	
85 90 95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu	
100 105 110	
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	384
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr	
115 120 125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile	
130 135 140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
145 150 155 160	
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
165 170 175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
180 185 190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
195 200 205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
210 215 220	

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Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
225 230 235 240	
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	
245 250 255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	
260 265 270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag	864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	
275 280 285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
290 295 300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
305 310 315 320	
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
325 330 335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
340 345 350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
355 360 365	
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Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp	
370 375 380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr	
385 390 395 400	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag	1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	
405 410 415	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata	1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile	
420 425 430	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata	1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile	
435 440 445	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat	1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn	
450 455 460	

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 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac ggt gtt gga 1488
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Gly Val Gly
 485 490 495

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 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 1584
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 1632
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
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aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 1680
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555 560

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 35 40 45
 Ala Ala Ile Asn Ser Asp Gly Gly Ile Thr Tyr Tyr Leu Asp Thr Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Phe Tyr Cys
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 115 120

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Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asn	Met	Gln	Ser
65					70					75				80	
Glu	Asp	Leu	Ala	Asp	Phe	Phe	Cys	Gln	Gln	Tyr	Ser	Asn	Tyr	Pro	Trp
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			100					105					110		
Pro	Thr	Val	Ser												
			115												